

in fitness, or a random population bottleneck. Sequencing of the entire virus genome of selected specimens is underway to ascertain the molecular basis to any differences in fitness among strains and to further analyze selection pressure and recombination for DEN-4.

14th Asia Pacific Military Medical Conference. Brisbane, Australia. 9-14 May 2004.

MOLECULAR EVOLUTION AND EPIDEMIOLOGY OF DENGUE-3 AND -4 VIRUSES IN BANGKOK, THAILAND

Zhang C, Klungthong C, Monkongdee P, Mammen MP Jr and Holmes EC

Sixty dengue-3 (DEN-3) and fifty-three dengue-4 (DEN-4) virus isolates from children in Bangkok with varying degrees of clinical dengue severity [dengue fever/dengue hemorrhagic fever/dengue shock syndrome (DF/DHF/DSS)] from 1973 to 2002 were selected to sequence virus envelope (E) and partial pre-membrane/membrane (preM/M) genes. An analysis of the results was completed to observe potential trends in molecular evolution and the epidemiology of circulating dengue viruses in Bangkok, Thailand. A new genotype of DEN-4 was defined in 5 of fifty-three isolates. This new genotype caused both DF (2 cases) and DHF/DSS (3 cases). Phylogenetic analysis showed that only genotype II of the DEN-3 virus serotype and genotype I (majority), IIA (1 case) and III (we defined) of the DEN-4 (5 cases) circulated in Bangkok, Thailand during the past three decades. There were no diagnostic sequence differences between DF and DHF/DSS, suggesting that E gene alone does not determine disease severity. The Phylogenetic trees indicated that strains of DEN-3 and the genotype I of DEN-4 virus circulating in Bangkok prior to 1990 appear to have disappeared and have been replaced by new lineages that have evolved locally, rather than being introduced. However, the genotype IIA of DEN-4 seems being introduced from the neighboring country of Malaysia. Sequencing virus entire genome of some selected samples for both DEN-3 and DEN-4 is undertaking for further analysis on selection pressure and recombination.

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MOLECULAR EVOLUTION AND EPIDEMIOLOGY OF DENGUE-3 VIRUSES IN BANGKOK, THAILAND

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Sixty dengue-3 viruses (DEN-3) isolated from children admitted between 1974 and 2002 in Bangkok, Thailand, with varying degrees of dengue [dengue fever/dengue hemorrhagic fever/dengue shock syndrome (DF/DHF/DSS)] were selected for sequencing of the envelope (E) gene to identify specific sequence patterns which may correlate with disease severity. Additionally, potential trends in molecular evolution and epidemiology of circulating DEN-3 viruses within Bangkok were explored. Phylogenetic analysis indicated that only genotype II circulated in

Bangkok during near past three decades. No specific sequence differences distinguished the DF and DHF isolates, suggesting that the E gene alone was not a determinant of disease severity. The phylogenetic tree revealed that there is a clear separation within the large Thai group of viruses, with a group virus strains from 1996 onwards being separated from the rest by a branch with 100% bootstrap support, the strains of DEN-3 virus circulating in Bangkok prior to 1996 appear to have disappeared and been replaced by new lineages that have evolved locally, rather than being introduced. However, it remains unclear and requires further study as to whether this replacement represents a selection event, so that strains differ in fitness, or a random population bottleneck. Sequencing of the entire virus genome of selected specimens is underway to ascertain the molecular basis to any differences in fitness among strains.

Abstract of the 10th International Workshop on Virus Evolution and Molecular Epidemiology. Helsinki, Finland. 30 August-3 September 2004. Abstract no. nr:4:6/60

Abstract of the 23rd Annual Meeting of the American Society of Virology. Montreal, Canada. 10 July 2004. Abstract no. W37-3:154-155.

MOLECULAR EVOLUTION AND EPIDEMIOLOGY OF DENGUE-3 VIRUSES IN THAILAND

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Sixty dengue-3 (DEN-3) virus isolates from children in Bangkok with varying degrees of clinical dengue severity [dengue fever/dengue hemorrhagic fever/dengue shock syndrome (DF/DHF/DSS)] from 1973 to the present were selected to sequence virus envelope (E) and partial pre-membrane/membrane (preM/M) genes. An analysis of the results was completed to observe potential trends in molecular evolution and the epidemiology of circulating dengue viruses in Thailand. Phylogenetic analysis indicated that only genotype II of the DEN-3 virus serotype circulated in Thailand during the past three decades. There were no diagnostic sequence differences between them, suggesting that E gene alone does not determine disease severity. Comparison of nucleic acid sequences of DEN-3 virus genotype II from Thailand with strains of DEN-3 virus genotype II from GenBank revealed that our 60 DEN-3 isolates share 96.3 – 99.7% nucleic acid sequence homology and 96.6 – 99.8% amino acid sequence homology. The Phylogenetic tree showed that strains of DEN-3 virus circulating in Thailand prior to 1990 appear to have disappeared and have been replaced by new lineages that have evolved locally, rather than being introduced. Sequencing virus entire genome of some selected samples is undertaking for further analysis on selection pressure and recombination.

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